

Serial Number: 09/308,830

ENTERED

#14 SK 8/16/00

1645

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

Input Set : A:\Pto.amc
Output Set: N:\CRF3\08102000\I308830.raw

SEQUENCE LISTING

```

C--> 5 (1) GENERAL INFORMATION:
7      (i) APPLICANT: Regents of the University of Minnesota
C--> 9      (ii) TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
10      AND METHODS OF USE
12      (iii) NUMBER OF SEQUENCES: 13
14      (iv) CORRESPONDENCE ADDRESS:
15          (A) ADDRESSEE: Merchant & Gould P.C.
16          (B) STREET: P.O. Box 2903
17          (C) CITY: Minneapolis
18          (D) STATE: MN
19          (E) COUNTRY: USA
20          (F) ZIP: 55402-0903
22      (v) COMPUTER READABLE FORM:
23          (A) MEDIUM TYPE: Diskette
24          (B) COMPUTER: IBM Compatible
25          (C) OPERATING SYSTEM: DOS
26          (D) SOFTWARE: FastSeq for Windows Version 2.0
28      (vi) CURRENT APPLICATION DATA:
C--> 29          (A) APPLICATION NUMBER: US/09/308,830
C--> 30          (B) FILING DATE: 04-Aug-1999
36          (C) CLASSIFICATION:
38      (vii) PRIOR APPLICATION DATA:
39          (A) APPLICATION NUMBER: PCT/US97/22228
40          (B) FILING DATE: 05-DEC-1997
41          (A) APPLICATION NUMBER: 60/032,930
42          (B) FILING DATE: 06-DEC-1996
44      (viii) ATTORNEY/AGENT INFORMATION:
45          (A) NAME: Skoog, Mark T
46          (B) REGISTRATION NUMBER: 40,178
47          (C) REFERENCE/DOCKET NUMBER: 600.346USWO
49      (ix) TELECOMMUNICATION INFORMATION:
50          (A) TELEPHONE: 612-332-5300
51          (B) TELEFAX: 612-332-9081
52          (C) TELEX:
57 (2) INFORMATION FOR SEQ ID NO: 1:
59      (i) SEQUENCE CHARACTERISTICS:
60          (A) LENGTH: 29 base pairs
61          (B) TYPE: nucleic acid
62          (C) STRANDEDNESS: single
63          (D) TOPOLOGY: linear
65      (ii) MOLECULE TYPE: Genomic DNA
67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69      CCATCACGGG TGGATTCTTG AAACAGGTG
71 (2) INFORMATION FOR SEQ ID NO: 2:
73      (i) SEQUENCE CHARACTERISTICS:
74          (A) LENGTH: 47 base pairs

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29

RAW SEQUENCE LISTING DATE: 08/10/2000
 PATENT APPLICATION: US/09/308,830 TIME: 18:06:36

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 Output Set: N:\CRF3\08102000\I308830.raw

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```

75      (B) TYPE: nucleic acid
76      (C) STRANDEDNESS: single
77      (D) TOPOLOGY: linear
79      (ii) MOLECULE TYPE: Genomic DNA
81      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
83  CCATCAGGCC CCCGTCGAC GATAAATAG TTGCTAAGCT ACAAGCT      47
85 (2) INFORMATION FOR SEQ ID NO: 3:
87      (i) SEQUENCE CHARACTERISTICS:
88          (A) LENGTH: 172 base pairs
89          (B) TYPE: nucleic acid
90          (C) STRANDEDNESS: single
91          (D) TOPOLOGY: linear
93      (ii) MOLECULE TYPE: Genomic DNA
95      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
97  CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
98  TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120
99  ATTTCCATAA ATATTAAATA ATAATTAAAA ATAAATAAT AAATAATTAA TC      172
102 (2) INFORMATION FOR SEQ ID NO: 4:
104      (i) SEQUENCE CHARACTERISTICS:
105          (A) LENGTH: 172 base pairs
106          (B) TYPE: nucleic acid
107          (C) STRANDEDNESS: single
108          (D) TOPOLOGY: linear
110      (ii) MOLECULE TYPE: Genomic DNA
112      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
114  CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
115  TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120
116  ATTTCCATAA ATATTAAATA ATAATTAAAA ATAAATAAT AAATAATTAA TC      172
118 (2) INFORMATION FOR SEQ ID NO: 5:
120      (i) SEQUENCE CHARACTERISTICS:
121          (A) LENGTH: 172 base pairs
122          (B) TYPE: nucleic acid
123          (C) STRANDEDNESS: single
124          (D) TOPOLOGY: linear
126      (ii) MOLECULE TYPE: Genomic DNA
128      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
130  CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
131  TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120
132  ATTTCCATAA ATATTAAATA ATAATTAAAA ATAAATAAT AAATAATTAA TC      172
134 (2) INFORMATION FOR SEQ ID NO: 6:
136      (i) SEQUENCE CHARACTERISTICS:
137          (A) LENGTH: 172 base pairs
138          (B) TYPE: nucleic acid
139          (C) STRANDEDNESS: single
140          (D) TOPOLOGY: linear
142      (ii) MOLECULE TYPE: Genomic DNA
144      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
146  CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
147  TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120

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RAW SEQUENCE LISTING DATE: 08/10/2000
 PATENT APPLICATION: US/09/308,830 TIME: 18:06:36

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\08102000\I308830.raw

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148 ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC      172
151 (2) INFORMATION FOR SEQ ID NO: 7:
153   (i) SEQUENCE CHARACTERISTICS:
154       (A) LENGTH: 172 base pairs
155       (B) TYPE: nucleic acid
156       (C) STRANDEDNESS: single
157       (D) TOPOLOGY: linear
159   (ii) MOLECULE TYPE: Genomic DNA
161   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
163 CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
164 TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120
165 ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC      172
167 (2) INFORMATION FOR SEQ ID NO: 8:
169   (i) SEQUENCE CHARACTERISTICS:
170       (A) LENGTH: 172 base pairs
171       (B) TYPE: nucleic acid
172       (C) STRANDEDNESS: single
173       (D) TOPOLOGY: linear
175   (ii) MOLECULE TYPE: Genomic DNA
177   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
179 CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
180 TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120
181 ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC      172
183 (2) INFORMATION FOR SEQ ID NO: 9:
185   (i) SEQUENCE CHARACTERISTICS:
186       (A) LENGTH: 172 base pairs
187       (B) TYPE: nucleic acid
188       (C) STRANDEDNESS: single
189       (D) TOPOLOGY: linear
191   (ii) MOLECULE TYPE: Genomic DNA
193   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
195 CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
196 TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120
197 ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC      172
200 (2) INFORMATION FOR SEQ ID NO: 10:
202   (i) SEQUENCE CHARACTERISTICS:
203       (A) LENGTH: 172 base pairs
204       (B) TYPE: nucleic acid
205       (C) STRANDEDNESS: single
206       (D) TOPOLOGY: linear
208   (ii) MOLECULE TYPE: Genomic DNA
210   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
212 CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
213 TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120
214 ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC      172
216 (2) INFORMATION FOR SEQ ID NO: 11:
218   (i) SEQUENCE CHARACTERISTICS:
219       (A) LENGTH: 31 base pairs
220       (B) TYPE: nucleic acid

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/308,830

DATE: 08/10/2000
 TIME: 18:06:36

Input Set : A:\Pto.amc
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221      (C) STRANDEDNESS: single
222      (D) TOPOLOGY: linear
224      (ii) MOLECULE TYPE: Genomic DNA
226      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
228      CCATCACGGG TGGATCCTTG AACAGGTGC A
230 (2) INFORMATION FOR SEQ ID NO: 12:
232      (i) SEQUENCE CHARACTERISTICS:
233          (A) LENGTH: 1851 base pairs
234          (B) TYPE: nucleic acid
235          (C) STRANDEDNESS: single
236          (D) TOPOLOGY: linear
238      (ii) MOLECULE TYPE: Genomic DNA
239      (ix) FEATURE:
241          (A) NAME/KEY: Coding Sequence
242          (B) LOCATION: 828...1580
243          (D) OTHER INFORMATION:
246      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
248      CCATCACGCA TCACCTCATGT TTGACAGCTT ATCATCGATA AGCTTACTTT TCGAATCAGG      60
249      TCTATCCTTG AACACGGTGC AACATAGATT AGGGCATGGA GATTTACCAG ACAACTATGA      120
250      ACGTATATAC TCACATCAGC CAATCGGCAA TTGATGACAT TGGAACTAAA TTCAATCAAT      180
251      TTGTTACTAA CAAGCAACTA GATTGACAAC TAATTCTCAA CAAACGTTAA TTTAACAACA      240
252      TTCAAGTAAC TCCCACCGAG TCCATCAATG CTTACCGTAA GTAATCATAA CTTACTAAAA      300
253      CCTTGTACA TCAAGGTTT TTCTTTTGT CTTGTTTCATG AGTTACCATA ACTTTCTATA      360
254      TTATGACAA CTAATTTGAC AACTCTCAA TTATTTTCT GTCTACTCAA AGTTTCTTTC      420
255      ATTTGATATA GTCTAATTCC ACCATCACTT CTTCCACTCT CTCTACCGTC ACAACTTCAT      480
256      CATCTCTCAC TTTTTCGTGT GGTAAACAT AATCAAATAT CTTTCCGTTT TTACGCACTA      540
257      TCGCTACTGT GTCACCTAAA ATATACCCCT TATCAATCGC TTCTTTAAAC TCATCTATAT      600
258      ATAACATATT TCATCCTCCT ACCTATCTAT TCGTAAAAAG ATAAAAATAA CTATTGTTTT      660
259      TTTTGTATT TTATAATAAA ATTATTAATA TAAGTTAATG TTTTAAAAA ATATACAATT      720
260      TTATCTATT TATAGTTAGC TATTTTTC TGTAGTAA TATTGGTGAA TTGTAATAAC      780
261      CTTTTAAAT CTAGAGGAGA ACCCAGATAT AAAATGGAGG AATATTA ATG GAA AAC      836
262                                     Met Glu Asn
263                                     1
265      AAT AAA AAA GTA TTG AAG AAA ATG GTA TTT TTT GTT TTA GTG ACA TTT      884
266      Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu Val Thr Phe
267      5 10 15
269      CTT GGA CTA ACA ATC TCG CAA GAG GTA TTT GCT CAA CAA GAC CCC GAT      932
270      Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln Asp Pro Asp
271      20 25 30 35
273      CCA AGC CAA CTT CAC AGA TCT AGT TTA GTT AAA AAC CTT CAA AAT ATA      980
274      Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu Gln Asn Ile
275      40 45 50
277      TAT TTT CTT TAT GAG GGT GAC CCT GTT ACT CAC GAG AAT GTG AAA TCT      1028
278      Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn Val Lys Ser
279      55 60 65
281      GTT GAT CAA CTT TTA TCT CAC CAT TTA ATA TAT AAT GTT TCA GGG CCA      1076
282      Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val Ser Gly Pro
283      70 75 80
285      AAT TAT GAT AAA TTA AAA ACT GAA CTT AAG AAC CAA GAG ATG GCA ACT      1124

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/308,830

DATE: 08/10/2000

TIME: 18:06:36

Input Set : A:\Pto.amc

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286 Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu Met Ala Thr
287      85          90          95
289 TTA TTT AAG GAT AAA AAC GTT GAT ATT TAT GGT GTA GAA TAT TAC CAT 1172
290 Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu Tyr Tyr His
291 100      105      110      115
293 CTC TGT TAT TTA TGT GAA AAT GCA GAA AGG AGT GCA TGT ATC TAC GGA 1220
294 Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys Ile Tyr Gly
295      120      125      130
297 GGG GTA ACA AAT CAT GAA GGG AAT CAT TTA GAA ATT CCT AAA AAG ATA 1268
298 Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro Lys Lys Ile
299      135      140      145
301 GTC GTT AAA GTA TCA ATC GAT GGT ATC CAA AGC CTA TCA TTT GAT ATT 1316
302 Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser Phe Asp Ile
303      150      155      160
305 GAA ACA AAT AAA AAA ATG GTA ACT GCT CAA GAA TTA GAC TAT AAA GTT 1364
306 Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp Tyr Lys Val
307      165      170      175
309 AGA AAA TAT CTT ACA GAT AAT AAG CAA CTA TAT ACT AAT GGA CCT TCT 1412
310 Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn Gly Pro Ser
311 180      185      190      195
313 AAA TAT GAA ACT GGA TAT ATA AAG TTC ATA CCT AAG AAT AAA GAA AGT 1460
314 Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu Ser
315      200      205      210
317 TTT TGG TTT GAT TTT TTC CCT GAA CCA GAA TTT ACT CAA TCT AAA TAT 1508
318 Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln Ser Lys Tyr
319      215      220      225
321 CTT ATG ATA TAT AAA GAT AAT GAA ACG CTT GAC TCA AAC ACA AGC CAA 1556
322 Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn Thr Ser Gln
323      230      235      240
325 ATT GAA GTC TAC CTA ACA ACC AAG TAAC TTTTGTG CTTTGGCAA CCTTACCTAC 1610
326 Ile Glu Val Tyr Leu Thr Thr Lys
327      245      250
329 TGCTGGATT AGAAATTTTA TTGCAATTCT TTTATTAATG TAAAAACCGC TCATTGATG 1670
330 AGCGGTTTTG TCTTATCTAA AGGAGCTTTA CCTCCTAATG CTGCAAAATT TTAAATGTTG 1730
331 GATTTTTGTA TTGTCTATT GTATTGTATG GGTAATCCCA TTTTTCGACA GACATCGTCG 1790
332 TGCCACCTCT AACACCAAAA TCATAGACAG GAGCTTGTAG CTTAGCAACT ATTTTATCGT 1850
333 C 1851
335 (2) INFORMATION FOR SEQ ID NO: 13:
337 (i) SEQUENCE CHARACTERISTICS:
338 (A) LENGTH: 251 amino acids
339 (B) TYPE: amino acid
340 (C) STRANDEDNESS: single
341 (D) TOPOLOGY: linear
343 (ii) MOLECULE TYPE: protein
344 (v) FRAGMENT TYPE: internal
346 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
348 Met Glu Asn Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu
349 1 5 10 15
350 Val Thr Phe Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/308,830

DATE: 08/10/2000
TIME: 18:06:37

Input Set : A:\Pto.amc
Output Set: N:\CRF3\08102000\I308830.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

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1645

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/308,830
 DATE: 08/08/2000
 TIME: 14:42:24
 Input Set : A:\Seqlist.txt
 Output Set: N:\CRF3\08082000\I308830.raw

SEQUENCE LISTING

C--> 5 (1) GENERAL INFORMATION:
 7 (i) APPLICANT: Regents of the University of Minnesota
 C--> 9 (ii) TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
 10 AND METHODS OF USE
 12 (iii) NUMBER OF SEQUENCES: 13
 14 (iv) CORRESPONDENCE ADDRESS:
 15 (A) ADDRESSEE: Merchant & Gould P.C.
 16 (B) STREET: P.O. Box 2903
 17 (C) CITY: Minneapolis
 18 (D) STATE: MN
 19 (E) COUNTRY: USA
 20 (F) ZIP: 55402-0903
 22 (v) COMPUTER READABLE FORM:
 23 (A) MEDIUM TYPE: Diskette
 24 (B) COMPUTER: IBM Compatible
 25 (C) OPERATING SYSTEM: DOS
 26 (D) SOFTWARE: FastSEQ for Windows Version 2.0
 28 (vi) CURRENT APPLICATION DATA:
 C--> 29 (A) APPLICATION NUMBER: US/09/308,830
 C--> 30 (B) FILING DATE: 04-Aug-1999
 36 (C) CLASSIFICATION:
 38 (vii) PRIOR APPLICATION DATA:
 34 (A) APPLICATION NUMBER: PCT/US97/22228
 35 (B) FILING DATE: 05-DEC-1997
 39 (A) APPLICATION NUMBER: 60/032,930
 40 (B) FILING DATE: 06-DEC-1996
 44 (viii) ATTORNEY/AGENT INFORMATION:
 45 (A) NAME: Skoog, Mark T
 46 (B) REGISTRATION NUMBER: 40,178
 47 (C) REFERENCE/DOCKET NUMBER: 600.346USWO
 49 (ix) TELECOMMUNICATION INFORMATION:
 50 (A) TELEPHONE: 612-332-5300
 51 (B) TELEFAX: 612-332-9081
 52 (C) TELEX:

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

335 (2) INFORMATION FOR SEQ ID NO: 13:
 337 (i) SEQUENCE CHARACTERISTICS:
 338 (A) LENGTH: 251 amino acids
 339 (B) TYPE: amino acid
 340 (C) STRANDEDNESS: single
 341 (D) TOPOLOGY: linear
 343 (ii) MOLECULE TYPE: protein
 344 (v) FRAGMENT TYPE: internal

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/308,830

DATE: 08/08/2000

TIME: 14:42:24

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\08082000\I308830.raw

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346      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
348 Met Glu Asn Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu
349      1          5          10          15
350 Val Thr Phe Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln
351      20          25          30
352 Asp Pro Asp Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu
353      35          40          45
354 Gln Asn Ile Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn
355      50          55          60
356 Val Lys Ser Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val
357      65          70          75          80
358 Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu
359      85          90          95
360 Met Ala Thr Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu
361      100         105         110
362 Tyr Tyr His Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys
363      115         120         125
364 Ile Tyr Gly Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro
365      130         135         140
366 Lys Lys Ile Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser
367      145         150         155         160
368 Phe Asp Ile Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp
369      165         170         175
370 Tyr Lys Val Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn
371      180         185         190
372 Gly Pro Ser Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn
373      195         200         205
374 Lys Glu Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln
375      210         215         220
376 Ser Lys Tyr Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn
377      225         230         235         240
378 Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr Lys
379      245         250

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E--> 386 7

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/308,830

DATE: 08/08/2000

TIME: 14:42:25

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\08082000\I308830.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:386 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:13

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